

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 13, 2001, 18:08:46 ; Search time 1088.91 Seconds
(without alignments)
12188.502 Million cell updates/sec

Title: US-09-481-990-1
Perfect score: 1894
Sequence: 1 GGGCAGGAGAGACGGCGCTGC.....ATATATAAAAAAAAAAAAA 1894

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 7991742 seqs, 3503743858 residues

Total number of hits satisfying chosen parameters: 15983484

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

EST:*

1: gb_est1:*
2: gb_est2:*
3: gb_est3:*
4: gb_est4:*
5: gb_est5:*
6: gb_est6:*
7: gb_est7:*
8: gb_est8:*
9: gb_est9:*
10: gb_est10:*
11: gb_est11:*
12: gb_est12:*
13: gb_est13:*
14: gb_est14:*
15: gb_est15:*
16: gb_est16:*
17: gb_est17:*
18: gb_est18:*
19: gb_est19:*
20: gb_est20:*
21: gb_est21:*
22: gb_est22:*
23: gb_est23:*
24: gb_est24:*
25: gb_est25:*
26: gb_est26:*
27: gb_est27:*
28: gb_est28:*
29: gb_est29:*
30: gb_est30:*
31: gb_est31:*
32: gb_est32:*
33: gb_est33:*
34: gb_est34:*
35: gb_est35:*
36: gb_est36:*
37: gb_est37:*
38: gb_est38:*
39: gb_est39:*
40: gb_est40:*
41: em_estda:*
42: em_estfun:*
43: em_esthum1:*

44: em_esthum2:*
45: em_esthum3:*
46: em_esthum4:*
47: em_esthum5:*
48: em_esthum6:*
49: em_esthum7:*
50: em_esthum8:*
51: em_esthum9:*
52: em_esthum10:*
53: em_esthum11:*
54: em_esthum12:*
55: em_esthum13:*
56: em_esthum14:*
57: em_esthum15:*
58: em_esthum16:*
59: em_esthum17:*
60: em_esthum18:*
61: em_esthum19:*
62: em_esthum20:*
63: em_estin1:*
64: em_estin2:*
65: em_estin3:*
66: em_estin4:*
67: em_estov1:*
68: em_estov2:*
69: em_estpl1:*
70: em_estpl2:*
71: em_estpl3:*
72: em_estpl4:*
73: em_estpl5:*
74: em_estro1:*
75: em_estro2:*
76: em_estro3:*
77: em_estro4:*
78: em_estro5:*
79: em_estro6:*
80: em_estro7:*
81: em_estro8:*
82: em_estro9:*
83: em_estro10:*
84: em_estro11:*
85: em_estro12:*
86: em_estro13:*
87: gb_esta1:*
88: gb_esta2:*
89: gb_esta3:*
90: gb_esta4:*
91: gb_esta5:*
92: gb_esta6:*
93: gb_esta7:*
94: gb_esta8:*
95: gb_esta9:*
96: gb_esta10:*
97: gb_esta11:*
98: gb_esta12:*
99: gb_esta13:*
100: gb_esta14:*
101: gb_esta15:*
102: gb_esta16:*
103: gb_esta17:*
104: gb_esta18:*
105: gb_esta19:*
106: gb_esta20:*
107: gb_esta21:*
108: gb_esta22:*
109: gb_esta23:*
110: gb_esta24:*
111: gb_esta25:*
112: em_esthum21:*
113: em_esthum22:*
114: em_esthum23:*
115: em_estom1:*
116: em_estom2:*

117: em_estp16:*
 118: em_estp17:*
 119: em_estp18:*
 120: em_estp19:*
 121: em_estp20:*
 122: em_estp21:*
 123: em_estp22:*
 124: em_estp23:*
 125: em_estp24:*
 126: em_estp25:*
 127: em_estp26:*
 128: em_estp27:*
 129: em_estp28:*
 130: em_estp29:*
 131: em_estp30:*
 132: em_estp31:*
 133: em_estp32:*
 134: em_estp33:*
 135: em_estp34:*
 136: em_estp35:*
 137: em_estp36:*
 138: em_estp37:*
 139: em_estp38:*
 140: em_estp39:*
 141: em_estp40:*
 142: em_estp41:*
 143: em_estp42:*
 144: em_estp43:*
 145: em_estp44:*
 146: em_estp45:*
 147: em_estp46:*
 148: em_estp47:*
 149: em_estp48:*
 150: em_estp49:*
 151: em_estp50:*
 152: em_estp51:*
 153: em_estp52:*
 154: em_estp53:*
 155: em_estp54:*
 156: em_estp55:*
 157: em_estp56:*
 158: em_estp57:*
 159: em_estp58:*
 160: em_estp59:*
 161: em_estp60:*
 162: em_estp61:*
 163: em_estp62:*
 164: em_estp63:*
 165: em_estp64:*
 166: em_estp65:*
 167: em_estp66:*
 168: em_estp67:*
 169: em_estp68:*
 170: em_estp69:*
 171: em_estp70:*
 172: em_estp71:*
 173: em_estp72:*
 174: em_estp73:*
 175: em_estp74:*
 176: em_estp75:*
 177: em_estp76:*
 178: em_estp77:*
 179: em_estp78:*
 180: em_estp79:*
 181: em_estp80:*
 182: em_estp81:*
 183: em_estp82:*
 184: em_estp83:*
 185: em_estp84:*
 186: em_estp85:*
 187: em_estp86:*
 188: em_estp87:*
 189: em_estp88:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	552.4	29.2	676	27	AI956397
2	538.4	28.4	676	27	AI956401
3	535.2	28.3	682	27	AI956216
4	531.6	28.1	586	1	AA001030
5	518	27.3	626	139	BF030864
6	497.6	26.3	681	107	BE377443
7	492.8	26.0	588	143	N78391
8	488	25.8	607	37	AV612885
9	477	25.2	602	13	AA872079
10	474	25.0	475	27	AI934807
11	454.2	24.0	484	26	AI924793
12	439.4	23.2	551	38	AW012076
13	419	22.1	742	106	BE309179
14	417.2	22.0	434	12	AA858126
15	414.4	21.9	424	1	AA021294
16	391.2	20.7	481	143	N51100
17	391	20.6	528	2	AA143352
18	385.8	20.4	471	145	T74333
19	385	20.3	385	7	AA408660
20	381.2	20.1	456	16	AI129709
21	376.2	19.9	518	111	BE720244
22	373	19.7	381	22	AI566688
23	372	19.6	421	95	AW784337
24	369.4	19.5	496	87	AW227291
25	369.4	19.5	412	106	BE284810
26	361.8	19.1	417	134	BE088384
27	359.6	18.9	563	24	AI770078
28	357.8	18.9	401	90	AA429512
29	352.6	18.6	417	21	AI493368
30	352.4	18.6	369	5	AA308453
31	333	17.6	343	5	AA307980
32	324.2	17.1	333	4	AA257164
33	319	16.8	539	38	AW012792
34	315.8	16.7	600	107	BE373364
35	314	16.6	536	146	T89472
36	312.4	16.5	315	147	Z39663
37	307.4	16.2	364	146	T89039
38	306.2	16.2	418	93	AW619432
39	298	15.7	537	20	AI425785
40	295	15.6	318	147	Z43599
41	281.8	14.9	298	140	F12504
42	280.2	14.8	353	142	N46450
43	279.4	14.8	285	140	F03207
44	279.4	14.8	604	139	BF046131
45	277.2	14.6	323	39	AW020278

ALIGNMENTS

RESULT 1
 AI956397
 LOCUS AI956397 676 bp mRNA
 DEFINITION u174906.y1 Sugano mouse kidney mRna Mus musculus cDNA clone
 IMAGE:2136346 5' similar to TR:000180 000180 POTASSIUM CHANNEL
 KCNOL.1 mRNA sequence.
 ACCESSION AI956397
 VERSION AI956397.1 GI:5749106
 KEYWORDS EST.

SOURCE	house mouse.
ORGANISM	Mus musculus
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. I (bases 1 to 676)
AUTHORS	Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y., Person ,B., Swaller,T., Gibbons,M., Page,D., Harvey,N., Schurk,R., Ritter ,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R., Waterston,R. and Wilson,R.
TITLE	The WashU-NCI Mouse EST Project 1999
JOURNAL	Unpublished (1999)
COMMENT	Contact: Marra M/WashU-NCI Mouse EST Project 1999 Washington University School of Medicine 444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA Tel: 314 286 1800 Fax: 314 286 1810 Email: mouseest@watson.wustl.edu This clone is available royalty-free through LNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information. MGI:1001022 Possible reversed clone; similarity on wrong strand Seq primer: custom primer used High quality sequence stop: 466. Location/Qualifiers 1..676
FEATURES	
SOURCE	

			/organism="Mus musculus"		
			/strain="C57BL"		
			/db.xref="taxon:10090"		
			/clone="IMAGE:2136346"		
			/clone_lib="Sugano mouse kidney mkia"		
			/sex="female"		
			/dev_stage="adult"		
			/lab_host="DH10B"		
			/note="Organ: kidney; Vector: pME18S-FL3; Site_1: DraIII		
			(CACTGTTGG); Site_2: DraIII (CACCAATGTG); 1st strand cDNA		
			was primed with an oligo(dT) primer		
			[ATGTGGCCCTTTTTTTTTTTTTTT]		
			ligated to a DraIII adaptor [TGTTGGCCCTACTGG], digested		
			and cloned into distinct DraIII sites of the pME18S-FL3		
			vector (5' site CACGTGTG, 3' site CACCAATGTG). XhoI should		
			be used to isolate the cDNA insert. Size selection was		
			performed to exclude fragments <1.5kb. Library		
			constructed by Dr. Sumio Sugano (University of Tokyo		
			Institute of Medical Science). Custom primers for		
			sequencing: 5' end primer CTTCGTGCCTTAAGACCTCGC and 3' end		
			primer CGACCTCTACACTCGACGACA."		
BASE COUNT	107 a	210 c	184 g	173 t	2 others
ALIGN					
Query Match		29.2%	Score 552.4;	DB 27;	Length 676;
Best Local Similarity		88.5%;	Pred. No. 2.3e-111;		
Matches 598;	Conservative	0;	Mismatches 78;	Indels	0;
Gaps					
Dd	263 GCTGGGCTAATTGCTCATCTACCTGCTGTGGGGCCAGCACTGCTTCCTCTGCTGGAGCTGCC	322			
	1 GCTGGGCTAACCCTTTCATCTGTGTTGGGCCCCCTGTGCTCTCTGTCCGTGGAGCTGCC	60			
Oy	333 CATAGAGACACTGCTGCGCCAGAGACTGCGCAAGCTGAAGCGACGCTTCTTGGAGAGACA	382			
	61 TTATGAGAGCACTGTGCGCCAGAGACTGTGGCGCAAGCTGAAGCGCGCTTCCTGGAGAGAGA	120			
Dd	383 CGAGTGCTGTGTAGACAGCACTGTGAGCAGTAGTCTCTGGGCCCAGTGCTGGAGCCAGCAA	442			
Dd	121 CGAGTGCTGTGTGAGCCGCGACAGCTGGAGAGATCTCTGGGCCCAGTGCTGGAGCCAGCAA	180			
Oy	443 CTACGCGCTGTGCTGTACAGCAAGCCTCGGGGCAACTGGAJACTGGAGACTTCACTCCGC	502			
Dd	181 TTATGAGAGTGTGCGTGTCAAGCAAGCCTCGGGAAATTTGGATTTGGAATTCACCTCGGC	240			
Oy	503 GCTCTTCTTCCGACACCGCTGCTCTCCACCAACAGGTTATGATCCACACCGTCCCTTGTG	562			

Db	241	GCTCTTCGTCCAGCAGCGTGCTGTCACCAAGAGCGTATGGCGCACAGCGGCCCTGTC	300
Oy	563	AGATGAGAGTAAGGCCTTTGCAATCATTAATCTCCGTCATGGCATTCCTTACCCTCT	622
Db	301	AGAATGGGGGAAACCTTTGCAATCATTAATCTGTCATCGGCAATCCGTTACCCCTCT	360
Oy	623	GTTCTGACGGCTGTGGTCCAGGCGAACCGGACGTCACCGGACCGGCGGCTCTTA	682
Db	361	CTTCTGACGGCGGTGGTCCAGGCGTACCGGTCACCGGTCACCGGACCGGCTCTTA	420
Oy	683	CTTCCACATCCGCTGGGGGCTTTCACAAGAGGTGGTGGCCATCTGTCATMGCCGCTCTCT	742
Db	421	CTTCCACATFAGCGTGGGGCTTTCACAAGAGGTGGTGGCCATTTGTCATMGCCGCTCTCT	480
Oy	743	TGGGTTGTGTCAGCTGTGTCGCTCTTCTTTCATCCCGCCGCGTGTCTCTCAGTCTGGA	802
Db	481	GAGATTGTGTACCGCTTTCCTGCTTCTTTCATCCAGCGCGGTGTCTGTCTGCTGGA	540
Oy	803	GGATGATCGAATCTCTCGAATCCTTTATTTTGTTTATTTCCCGAGACCATTTGG	862
Db	541	GGATGATCGAATCTCTCGAATCCTTTATTTTGTTTATTTCCCGAGACCATTTGG	600
Oy	863	CCTGGGGATTAATGTGCTGGGAGAGGCTPACATCAAATAATCAGAGACTTATATGAT	922
Db	601	CCTGGGGATTAATGTGCTGGGAGAGGCTPACATCAAATAATCAGAGACTTATATGAT	660
Oy	923	TGGGATCAGCTGTTAC	938
Db	661	CGTATCATCGTGTAC	676
RESULT	2		
A1956401			
LOCUS	A1956401	676 bp	mRNA EST
DEFINITION	U174911.Y1 Sugano mouse kidney mRna Mus musculus cDNA clone IMAGE:2136356.5 similar to TR-000180 000180 POTASSIUM CHANNEL KCNO1.; mRNA sequence.		
VERSION	A1956401		
KEYWORDS	A1956401.1 GI:5749110		
SOURCE	EST.		
ORGANISM	house mouse.		
REFERENCE	Mus musculus		
AUTHORS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus; 1 (bases 1 to 676)		
TITLE	Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y., Pearson,B., Swaller,T., Gibbons,M., Pepe,D., Harvey,N., Schurr,R., Ritten,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R., Waterston,R. and Wilson.R.		
JOURNAL	The WashU-NCI Mouse EST Project 1999		
COMMENT	Unpublished (1999) Contact: Marra M/WashU-NCI Mouse EST Project 1999 Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA Tel: 314 286 1800 Fax: 314 286 1810 Email: mouseest@wustl.edu This clone is available royalty-free through LNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. MGI:1001032 Possible reversed clone: similarity on wrong strand Seq primer: custom primer used High quality sequence stop: 519. Location/Qualifiers 1..676 /organism="Mus musculus" /strain="C57BL" /db_xref="taxon:10090" /clone="IMAGE:2136356" /clone_lib="Sugano mouse kidney mRna" /sex="female" /dev_stage="adult"		

SOURCE
ORGANISM Bos taurus
COW.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovidae; Bovinae; Bos.
REFERENCE 1 (bases 1 to 607)
Sugimoto, Y., Hirotsune, S., Takasuga, A., Itoh, R., Jitohzono, A. and Suzuki, H.
TITLE bovine cDNA sequencing
JOURNAL Unpublished (2000)
COMMENT Contact: Yoshikazu Sugimoto
Animal Genetics Division
Shirakawa Institute of Animal Genetics
Oakura, Nishigo, Nishi-Shirakawa, Fukushima 961-8061, Japan
Tel: 81-248-25-5641
Fax: 81-248-25-5725
Email: kazusugi@cocoa.ocn.ne.jp
Single pass sequencing.
This clone was obtained from a polyA-deleted cDNA library.
FEATURES
source
Location/Qualifiers
1. 607
/organism="Bos taurus"
/db_xref="taxon:9913"
/clone_lib="Bos taurus lung fetus"
/tissue_type="lung"
/dev_stage="fetus"
/lab_host="DH10B"
/note="Vector: pZLI; Site: 1; SalI; Site: 2; NotI; Poly A
was deleted from a NotI site"
BASE COUNT 118 a 184 c 148 g 157 t
ORIGIN

Query Match 25.8%; Score 488; DB 37; Length 607;
Best Local Similarity 89.8%; Pred. No. 3.5e-97;
Matches 53; Conservative 0; Mismatches 60; Indels 1; Gaps 1;

468 GCGTCGGGCACTGGAAGTGGAGTCCGCGCTCTCTTCTGCGCAGACCGCTCTC 527
|||||
12 GCGTCGGGCACTGGAAGTGGAGTCCGCGCTCTCTTCTGCGCAGACCGCTCTC 71
|||||
528 TCACCCAGAGTTATGGCCACACCGCTGCTTCTCAATGAGAGTAAAGCCTTGCATC 587
|||||
72 TCACCCAGAGTTATGGCCACACCGCTGCTTCTCAATGAGAGTAAAGCCTTGCATC 131
|||||
588 ATCTACCCGCTATGGCATCCCTTCAACCTCTCTGTTCTCGAGAGGCTGATCCAGCGC 647
|||||
132 ATCTATTCGCTATGGCATCCCTTCAACCTCTCTGTTCTCGAGAGGCTGATCCAGCGT 191
|||||
648 ATACCGTGCAGCTACCGCGAGCGGCTCTCTTCTCAATGAGAGTAAAGCCTTCTC 707
|||||
192 GTTACCATCATGTCACCGGAGCGAGTCTCTTCTCAATGAGAGTAAAGCCTTCTC 251
|||||
708 AAGCAGTGGTGGCATTCATGCGCTGCTCTTCTGAGTTCATGCTGCTCTC 767
|||||
252 AAGCAGCAGTGGCATTCATGCGCTGCTCTTCTGAGTTCATGCTGCTCTC 311
|||||
768 TTTCTTACCCGGCGGCTGCTCTCTGAGTTCATGCGCTGAGTTCATGCGCTGAGTTC 827
|||||
312 TTTCTTACCCGGCGGCTGCTCTCTGAGTTCATGCGCTGAGTTCATGCGCTGAGTTC 371
|||||
828 TTTTATTTTGTATTTCTTCTGAGCAGATTTGGCTGAGTTCATGCGCTGAGTTC 887
|||||
372 TTTTATTTTGTATTTCTTCTGAGCAGATTTGGCTGAGTTCATGCGCTGAGTTC 431
|||||
888 GCGTACATCAAAAATTCAGAGAGCTTATAGATTGGATCAGCTTACCTGACTT 947
|||||
432 GGTTCATCATCAAAAATTCAGAGAGCTTATAGATTGGATCAGCTTACCTGACTT 491
|||||
948 GCGCTTATTCATGATGTTGTTCTGAAACCTTCTGTAACCTGAGCTGAAAGAA 1007
|||||
492 GGTCTCATTCGATGTTGGTGTCTGAAACCTTCTGTAACCTGAGCTGAAAGAA 551
|||||

QY 1008 TTCAGAAAAATGTTCTATGTGAGACAGACAGACG-AGGATCAGTGCACATCA 1062
|||||
Db 552 TTCAGAAAAATGTTCTATGTGAGACAGACAGACAGACAGATCAATGCACATCA 607
|||||

RESULT 9
AA872079/c
LOCUS
DEFINITION
AA872079 602 bp mRNA EST 17-MAR-1998
0112407.s1 NCI-CGAP GC4 Homo sapiens cDNA clone IMAGE:1476276 3'
similar to TR:000180 000180 PORASSIUM CHANNEL KCNO1.; mRNA
sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Homo sapiens
human.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (bases 1 to 602)
NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL
COMMENT
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert.Strausberg@nih.gov
Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael
Emmett-Buck, M.D., Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/biopr/image/image.html
Seq primer: -40m13 fwd. RT from Amersham
High quality sequence stop: 78.
FEATURES
source
Location/Qualifiers
1. 602
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:1476276"
/clone_lib="NCI-CGAP_GC4"
/tissue_type="pooled germ cell tumors"
/lab_host="DH10B"
/note="Vector: pTZ19-Pac (Pharmacia) with a modified
polylinker; 1st strand cDNA was prepared from 3 pooled
germ cell tumors, and was then primed with a Not I and Eco
oligo(dT) primer. Double-stranded cDNA was ligated to Eco
RI adaptors (Pharmacia), digested with Not I and cloned
into the Not I and Eco RI sites of the modified pTZ19
vector. Library is normalized. Library was constructed by
Bento Soares and M. Fatima Bonaldo."

BASE COUNT 159 a 137 c 124 g 182 t
ORIGIN

Query Match 25.2%; Score 477; DB 13; Length 602;
Best Local Similarity 90.9%; Pred. No. 9.2e-95;
Matches 552; Conservative 0; Mismatches 50; Indels 5; Gaps 4;

QY 978 ACCTTCTGTAACCTCATGAGCTGAAAAATTCAGAAAAATGTTCTATGTGAAGAGAC 1037
|||||
Db 602 ACCCTGTGTGACATCATGAGCT--AAAAATGAGATATG--TCATGTGAAG-ACGAC 547
|||||
QY 1038 AAGCAGCAGATCAGGTGACATCATGAGCAGTACCACTGCTCTCTCTGATCACA 1097
|||||
Db 546 GACGCGCATATCAGGTGACATCATGAGCAGTACCACTGCTCTCTCTGATCACA 487
|||||
QY 1098 GACGAGCAGCTGAGCAAGAAAGAGCAGAGCAAAATGAGCTTTTGGGCACCCAG 1157
|||||
Db 486 GACGAGCAGCTGAGCAAGAAAGAGCAGAGCAAAATGAGCTTTTGGGCACCCAG 427
|||||

		/issue-type="anaplastic oligodendroglioma" /lab_host="DH10B" /note="Organ: brain; Vector: pT73d-Pac (Pharmacia) with a modified polylinker; Site.1: Not I; Site.2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5' TGTTACCAATCTGAACTGGAGGAGCGCCGCATAGGTCTTTTTTTTTTTTTTTT T 3']; double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT73 vector. Library is normalized, and was constructed by Bento Soares and M.Fatima Bonaldo."
BASE COUNT	122 a 117 c 92 g 144 t	
ORIGIN		
Query Match	Best Local Similarity 25.0%; Score 474; DB 27; Length 475;	
Matches 474; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
OY	864 CTGGGGGATTATGTGCCCTGGGGGAAGGCTACATCAATAAATTCAGAGACTCTATTAAGATT	923
DB	475 CTGGGGGATTATGTGCCCTGGGGGAAGGCTACATCAATAAATTCAGAGACTCTATTAAGATT	416
OY	924 GGGATCAGCTGTGTACCTCTACTTGCCCTTATGTGCATGTTGGTAGTTCCTGAAAACCTTC	983
DB	415 GGGATCAGCTGTGTACCTCTACTTGCCCTTATGTGCATGTTGGTAGTTCCTGAAAACCTTC	356
OY	984 TGTGAACCTCATGACCTGAAAAAATTCGAAAAAATGTTCTATGTGAAACAAGACAAAGGAC	1043
DB	355 TGTGAACCTCATGACCTGAAAAAATTCGAAAAAATGTTCTATGTGAAACAAGACAAAGGAC	296
OY	1044 GAGGATCAGGTGCACATCATAGAGCATGACCACACTGTCCTCTCTCGATCACAGACCAG	1103
DB	295 GAGGATCAGGTGCACATCATAGAGCATGACCACACTGTCCTCTCTCGATCACAGACCAG	236
OY	1104 GCAGCTGCATGAAAGAAGACGACAGCAAATATGAGCTTTTGTGGCCACCAGTCATCT	1163
DB	235 GCAGCTGCATGAAAGAAGACGACAGCAAATATGAGCTTTTGTGGCCACCAGTCATCT	176
OY	1164 GCCCTCGTGAAATGGCCCTGCACAACCATTTGAGCGTATGTTGGCATTTATGCTTAGAGCA	1223
DB	175 GCCCTCGTGATGACCTCTGCACAAACCATTTGAGCGTATGTTGGCATTTATGCTTAGAGCA	116
OY	1224 CCAGGCTAGGGTGCACAAGAGAGGCTTAAGTATGTTTATTTTATTCAGAAATGCAAAAGC	1283
DB	115 CCAGGCTAGGGTGCACAAGAGAGGCTTAAGTATGTTTATTTTATTCAGAAATGCAAAAGC	56
OY	1284 GAAATTTATGTCACTTTAAGAAATATGCTACTGTTTGCAATGCTTATTTAAAAA	1337
DB	55 GAAATTTATGTCACTTTAAGAAATATGCTACTGTTTGCAATGCTTATTTAAAAA	2
RESULT 11		
LOCUS	A1924793/c	
DEFINITION	wn33a04.x1 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2446254 3'	
ACCESSION	A1924793	
VERSION	A1924793.1 GI:5660757	
KEYWORDS	EST.	
SOURCE	human.	
ORGANISM	Homo sapiens	
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.	
TITLE	NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.	
JOURNAL	National Cancer Institute, Cancer Genome Anatomy Project (CGAP),	
COMMENT	Unpublished (1997)	
	Contact: Robert Strausberg, Ph.D.	
	Tel: (301) 496-1550	
	Email: Robert.Strausberg@nih.gov	
	Tissue Procurement: Christopher Moskalko, M.D., Ph.D., Michael R.	

Db 278 GCCGACGTGAGACAGTTCCTGGGCCGCGTGTGAGAGCCACAAATATGAGATGCGGT 337
 QY 458 GGTGACAAAGCGCTGGGCAACTGGAACTTGACACTCCGGCTCTTCTGGCCAG 517
 Db 338 GGTGACAAAGCGCTGGGCAAAATGGAAATGGAGCTTACACTGGGCGCTTCTGGCCAG 397
 QY 518 CACCGTCTCTCCACACAGAGTTATGGCCACACCGCTTGTGATGAGATGAGAGC 577
 Db 398 CACCGTCTCTCCACACAGAGTTATGGCCACACCGCTTGTGATGAGATGAGAGC 457
 QY 578 CTCTGCAATCATCTACTCCGTCATTCGATTCCTTACCTCTGTTCTGAGGCTGT 637
 Db 458 CTCTGCAATCATCTACTCTGTCATGCGATCCGTTACCTCTGTTCTGAGGCTGT 517
 QY 638 GGTCCAGGCAATCAGCGTGCAGTGCAGCCGCGAG 670
 Db 518 GGTCCAGGCGTGCAGCGTGCAGTGCAGCCGCGAG 550

RESULT 13
 LOCUS BE309179 742 bp mRNA EST 13-JUL-2000
 DEFINITION 601095044F1 NCI_CGAP_Mam5 Mus musculus cDNA clone IMAGE:3489466 5',
 mRNA sequence.
 ACCESSION BE309179
 VERSION BE309179.1 GI:9166970
 KEYWORDS EST.
 SOURCE house mouse.
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 REFERENCE NIH-MGC http://www.ncbi.nlm.nih.gov/MGC/
 AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
 TITLE Unpublished (1999)
 JOURNAL Contact: Robert Strausberg, Ph.D.
 COMMENT Tel: (301) 496-1550
 Email: Robert.Strausberg@nih.gov
 Tissue Procurement: Lothar Hennighausen Ph.D., Robin Humphreys
 cDNA Library Preparation: Life Technologies, Inc.
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/MLN at:
 http://image.llnl.gov
 Plate: LHAM8530 row: h column: 11
 High quality sequence stop: 541.
 Location/Qualifiers
 1..742
 /organism="Mus musculus"
 /strain="C57/B6"
 /db_xref="taxon:10090"
 /clone="IMAGE:3489466"
 /clone_1db="NCI_CGAP_Mam5"
 /tissue_type="tumor, gross tissue"
 /dev_stage="7 months"
 /lab_host="DH10B"
 /note="Organ: mammary; Vector: pCMV-SPORT6; Site_1: SalI;
 Site_2: NotI; Cloned unidirectionally. Primer: Oligo dt.
 Library constructed by Life Technologies. Investigators
 providing samples: Lothar Hennighausen/Robin Humphreys,
 NIH"

BASE COUNT 144 a 217 c 202 g 179 t
 ORIGIN
 Query Match 22.1%; Score 419; DB 106; Length 742;
 Best Local Similarity 85.8%; Pred. No. 5.6e-12;
 Matches 500; Conservative 0; Mismatches 80; Indels 3; Gaps 3;

QY 455 GGTGCTGACAAAGCGCTGGGCAAC-TGGAACCTGGAGCTTCCGCGCTCTTCTG 513
 Db 1 GGTGCTGACAAAGCGCTGGGCAACATGGAATGGAGCTTCCGCGCTCTTCTG 60

QY 514 CCAGACCGCTGCTCCACACAGGTTATGGCCACACCGCTTGTGCAGATGAGAGTA 573
 Db 61 CCAGACCGCTGCTCCACACAGGTTATGGCCACACCGCTTGTGCAGATGAGAGTA 120
 QY 574 AGGCGTCTGCAATCATCTCTCGATTCGATTCGATTCGATTCGATTCGATTCGATTC 633
 Db 121 AAGCGTCTGCAATCATCTCTCGATTCGATTCGATTCGATTCGATTCGATTCGATTC 180
 QY 634 CTGTGCTCAGGCAATCAGCTGACAGTCCAGCCGAGCGCGCTCTTCTTCCATATCC 693
 Db 181 CCGTGTCCAGGCTGACAGTCCAGCTGACAGTCCAGCCGAGCGCGCTCTTCTTCCATATCC 240
 QY 694 GCTGGGCGCTTCCAAAGAGGTGTGGCCATGCTCATCCGCTGCTTGGGTTGTGA 753
 Db 241 GCTGGGCGCTTCCAAAGAGGTGTGGCCATGCTCATCCGCTGCTTGGGTTGTGA 300
 QY 754 CTGTGCTCAGGCAATCAGCTGACAGTCCAGCCGAGCGCGCTCTTCTTCCATATCC 813
 Db 301 CCGTGTCCAGGCTGACAGTCCAGCTGACAGTCCAGCCGAGCGCGCTCTTCTTCCATATCC 360
 QY 814 ACTTCCCTGGAATCCTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTT 873
 Db 361 ACTTCCCTGGAATCCTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTT 420
 QY 874 ATGTGCTGGGCAAGCTCATCAATCAAAATTCAGAGAGCTCTATAGATTGGATACGT 933
 Db 421 ATGTGCTGGGCAAGCTCATCAATCAAAATTCAGAGAGCTCTATAGATTGGATACGT 479
 QY 934 GTTACTCTGATCTTGGCCCTTATTTGATCTTGTGATCTTGTGAAACCTTGTGAACTCC 993
 Db 480 GTTACTCTGATCTTGGCCCTTATTTGATCTTGTGATCTTGTGAAACCTTGTGAACTCC 538
 QY 994 ATGAGCTGAAAAAATTCAGAAAAATGTTCTATGTGAAGAAGA 1036
 Db 539 ACGAGCTGAAAAAAGTCCAGAGAGTGTAGTGAAGAAAGGA 581

RESULT 14
 LOCUS AA858126/c
 DEFINITION 0656h07.s1 NCI_CGAP_Co8 Homo sapiens cDNA clone IMAGE:1435261 3',
 similar to TR:000180 000180 POTASSIUM CHANNEL KCNOL1., mRNA
 sequence.
 ACCESSION AA858126 434 bp mRNA EST 21-APR-1998
 VERSION AA858126
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 434)
 AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
 TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index
 JOURNAL Unpublished (1997)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Tel: (301) 496-1550
 Email: Robert.Strausberg@nih.gov
 Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
 Emmert-Buck, M.D., Ph.D.
 cDNA Library Preparation: M. Bento Soares, Ph.D.
 DNA Sequencing by: Washington University Genome Sequencing Center
 Clone distribution: NCI-CGAP clone distribution information can be
 found through the I.M.A.G.E. Consortium/MLN at:
 www-bio.llnl.gov/dbtrp/image/image.html
 Insert Length: 1249 Std Error: 0.00
 Seq primer: ~40m13 fwd. Et from Amersham
 High quality sequence stop: 392.
 Location/Qualifiers
 1..434
 /organism="Homo sapiens"

```

/db_xref="taxon:9606"
/clone_image="1435261"
/clone_lib="NCI_CGAP_C08"
/tissue_type="adenocarcinoma"
/lab_host="DH10B"
/notes="Organ: colon; Vector: pT73D-Pac (Pharmacia) with a
modified polylinker; 1st strand cDNA was prepared from
colon adenocarcinoma, and was then primed with a Not I -
oligo(dt) primer. Double-stranded cDNA was ligated to Eco
RI adaptors (Pharmacia), digested with Not I and cloned
into the Not I and Eco RI sites of the modified pT73
vector. Library is normalized. Library was constructed by
Bento Soares and M. Fatima Bonaldo."
BASE COUNT      113 a      104 c      87 g      130 t
ORIGIN

```

[illegible]

TITLE	Generation and analysis of 280,000 human expressed sequence tags
JOURNAL	Genome Res. 6 (9), 807-828 (1996)
MEDLINE	97044478
COMMENT	Contact: Wilson RK

Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: est@watson.wustl.edu
 This clone is available royalty-free through LNL : contact the
 IMAGE Consortium (lnl@image.lnl.gov) for further information.
 Insert Length: 1471 Std Error: 0.00
 Seq primer: -28M13 rev2 from Amersham
 High quality sequence stop: 383.
 Location/Qualifiers

FEATURES					
	Location/Qualifiers				
	1...424				
	/organism="Homo sapiens"				
	/db_xref="GDB:128085"				
	/db_xref="taxon:9606"				
	/clone="IMAGE:364182"				
	/clone_id="Soares retina N2b4HR"				
	/sex="male"				
	/tissue_type="retina"				
	/dev_strage="55 year old"				
	/lab_host="DH10B (ampicillin resistant)"				
	/note="Organ: eye; Vector: pRT73D (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5' TGTTACCAATCTGAAGTGCGGGCGCGCGGTCTTTTTTTTTTTTTTTT 3'], double-stranded cDNA was size selected, ligated to Eco RI adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pRT73 vector (Pharmacia). The retinas were obtained from a 55 year old Caucasian and total cellular poly(A)+ RNA was extracted 6 hrs after their removal. The retina RNA was kindly provided by Roderick R. McInnes M.D. Ph.D. from the University of Toronto. Library constructed by Bento Soares and M.Fatima Bonaldo."				
BASE COUNT	73 a	121 c	101 g	129 t	
ORIGIN					
Query Match	21.9%:	Score 414.4:	DB 1:	Length 424;	
Best Local Similarity	98.6%:	Pred. No. 5.2e-81;			
Matches 418:	Conservative	0:	Mismatches 6:	Indels 0:	Gaps 0:
OY	583 GCATCATCTACTCCGTCATTGGCATTCCTTACCCTCCTGTCTCTGACGGCTGTGATGC	642			
Dd	1 GCATCATCTACTCCGTCATTGGCATTCCTTACCCTCCTGTCTCTGACGGCTGTGATGC	60			
OY	643 AGCGATATACCGTGTGACGTCAACCCGAGCGCGTCTTACTTCCACATCCGCTGGGCT	702			
Dd	61 AGCGATATACCGTGTGACGTCAACCCGAGCGCGTCTTACTTCCACATCCGCTGGGCT	120			
OY	703 TCTCCAACGAGTGTGGCATTGTCATGTCATGTCGTCCTCTGGATTTTCTACTGTGTCT	762			
Dd	121 TCTCCAACGAGTGTGGCATTGTCATGTCATGTCGTCCTCTGGATTTTCTACTGTGTCT	180			
OY	763 GCTTCTTCTTCAATCCCGGCCGCTGTCTTCTCAAGTCTTGGAGATGATCGAATTCCTCG	822			
Dd	181 GCTTCTTCTTCAATCCCGGCCGCTGTCTTCTCAAGTCTTGGAGATGATCGAATTCCTCG	240			
OY	823 AATCCTTTATTTTGTATTATTTCCGAGACACATTGGCTGGGGATATATGCGCTG	882			
Dd	241 AATCCTTTATTTTGTATTATTTCCGAGACACATTGGCTGGGGATATATGCGCTG	300			
OY	883 GGGAAGGCTACAAATTCAGAGAGCTCTATAAGATTGGGATCACGTATTACCTGC	942			
Dd	301 GGGAAGGCTACAAATTCAGAGAGCTCTATAAGATTGGGATCACGTATTACCTGC	360			
OY	943 TACTTGGGCTTAATGGCATTTGGTAGATTTCGGAACCTTCTGTGAACCTCATGAGCTGA	1002			
Dd	361 TACTTGGGCTTAATGGCATTTGGTAGATTTCGGAACCTTCTGTGAACCTCATGAGCTGA	420			

Wed Feb 21 15:16:09 2001

us-09-481-990-1.rst

Page 13

Qy 1003 AAAA 1006
| | |
Db 421 AAAA 424

Search completed: February 14, 2001, 02:55:31
Job time: 31605 sec

THIS PAGE BLANK (USPTO)